

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/549,317  
Source: IFWJ0  
Date Processed by STIC: 6/30/06

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IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/549,317

DATE: 06/30/2006  
TIME: 10:10:34

Input Set : A:\81356247\_APP  
Output Set: N:\CRF4\06302006\J549317.raw

3 <110> APPLICANT: SOEJIMA, KENJI  
4 NAKAGAKI, TOMOHIRO  
5 MATSUMOTO, MASANORI  
6 FUJIMURA, YOSHIHIRO  
8 <120> TITLE OF INVENTION: CONSTRUCT COMPRISING REGION RECOGNIZED BY ANTIBODY  
9 AGAINST VON WILLEBRAND FACTOR-SPECIFIC CLEAVING  
10 PROTEASE  
12 <130> FILE REFERENCE: 81356/247  
14 <140> CURRENT APPLICATION NUMBER: 10/549,317  
15 <141> CURRENT FILING DATE: 2005-09-16  
17 <150> PRIOR APPLICATION NUMBER: PCT/JP04/003602  
18 <151> PRIOR FILING DATE: 2004-03-17  
20 <150> PRIOR APPLICATION NUMBER: JP 2003/71979  
21 <151> PRIOR FILING DATE: 2003-03-17  
23 <160> NUMBER OF SEQ ID NOS: 21  
25 <170> SOFTWARE: PatentIn Ver. 3.3  
27 <210> SEQ ID NO: 1  
28 <211> LENGTH: 1427  
29 <212> TYPE: PRT  
30 <213> ORGANISM: Homo sapiens  
32 <400> SEQUENCE: 1  
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34 1 5 10 15  
36 Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His  
37 20 25 30  
39 Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser  
40 35 40 45  
42 Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly  
43 50 55 60  
45 Phe Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu  
46 65 70 75 80  
48 His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His  
49 85 90 95  
51 Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala  
52 100 105 110  
54 Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu  
55 115 120 125  
57 Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr  
58 130 135 140  
60 Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr  
61 145 150 155 160  
63 Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu  
64 165 170 175

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66 Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val  
67 180 185 190  
69 Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys  
70 195 200 205  
72 Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His  
73 210 215 220  
75 Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser  
76 225 230 235 240  
78 Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro  
79 245 250 255  
81 Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser  
82 260 265 270  
84 Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro Pro Arg Pro  
85 275 280 285  
87 Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln Pro Gly Leu Tyr  
88 290 295 300  
90 Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val  
91 305 310 315 320  
93 Ala Cys Thr Phe Ala Arg Glu His Leu Asp Met Cys Gln Ala Leu Ser  
94 325 330 335  
96 Cys His Thr Asp Pro Leu Asp Gln Ser Ser Cys Ser Arg Leu Leu Val  
97 340 345 350  
99 Pro Leu Leu Asp Gly Thr Glu Cys Gly Val Glu Lys Trp Cys Ser Lys  
100 355 360 365  
102 Gly Arg Cys Arg Ser Leu Val Glu Leu Thr Pro Ile Ala Ala Val His  
103 370 375 380  
105 Gly Arg Trp Ser Ser Trp Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys  
106 385 390 395 400  
108 Gly Gly Gly Val Val Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro  
109 405 410 415  
111 Ala Phe Gly Gly Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met  
112 420 425 430  
114 Cys Asn Thr Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln  
115 435 440 445  
117 Gln Cys Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly  
118 450 455 460  
120 Ala Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp  
121 465 470 475 480  
123 Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile Met  
124 485 490 495  
126 Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro Ser Gly  
127 500 505 510  
129 Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly Ser Cys Arg  
130 515 520 525  
132 Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln Val Trp Asp Arg  
133 530 535 540  
135 Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys Ser Pro Arg Lys Gly  
136 545 550 555 560  
138 Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr Val Thr Phe Leu Thr Val

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139	565	570	575	
141	Thr Pro Asn Leu Thr Ser Val Tyr Ile Ala Asn His Arg Pro Leu Phe			
142	580	585	590	
144	Thr His Leu Ala Val Arg Ile Gly Gly Arg Tyr Val Val Ala Gly Lys			
145	595	600	605	
147	Met Ser Ile Ser Pro Asn Thr Thr Tyr Pro Ser Leu Leu Glu Asp Gly			
148	610	615	620	
150	Arg Val Glu Tyr Arg Val Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu			
151	625	630	635	640
153	Glu Glu Ile Arg Ile Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln			
154	645	650	655	
156	Val Tyr Arg Arg Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp			
157	660	665	670	
159	Ile Thr Phe Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp			
160	675	680	685	
162	Ala Ala Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg			
163	690	695	700	
165	Trp Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu			
166	705	710	715	720
168	Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu Ala			
169	725	730	735	
171	Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp Phe Gly			
172	740	745	750	
174	Pro Cys Ser Ala Ser Cys Gly Gly Leu Arg Glu Arg Pro Val Arg			
175	755	760	765	
177	Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu Pro Pro Ala Arg			
178	770	775	780	
180	Cys Arg Ala Gly Ala Gln Pro Ala Val Ala Leu Glu Thr Cys Asn			
181	785	790	795	800
183	Pro Gln Pro Cys Pro Ala Arg Trp Glu Val Ser Glu Pro Ser Ser Cys			
184	805	810	815	
186	Thr Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys Val			
187	820	825	830	
189	Pro Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly Ser			
190	835	840	845	
192	Val Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys			
193	850	855	860	
195	Pro Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala			
196	865	870	875	880
198	Pro Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val			
199	885	890	895	
201	Trp Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu			
202	900	905	910	
204	Met Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val			
205	915	920	925	
207	Gln Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu			
208	930	935	940	
210	Val Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala			
211	945	950	955	960

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213 Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr  
214 965 970 975  
216 Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu Asp  
217 980 985 990  
219 Thr Gln Cys Gln Gly Leu Pro Arg Pro Glu Pro Gln Glu Ala Cys Ser  
220 995 1000 1005  
222 Leu Glu Pro Cys Pro Pro Arg Trp Lys Val Met Ser Leu Gly Pro Cys  
223 1010 1015 1020  
225 Ser Ala Ser Cys Gly Leu Gly Thr Ala Arg Arg Ser Val Ala Cys Val  
226 1025 1030 1035 1040  
228 Gln Leu Asp Gln Gly Gln Asp Val Glu Val Asp Glu Ala Ala Cys Ala  
229 1045 1050 1055  
231 Ala Leu Val Arg Pro Glu Ala Ser Val Pro Cys Leu Ile Ala Asp Cys  
232 1060 1065 1070  
234 Thr Tyr Arg Trp His Val Gly Thr Trp Met Glu Cys Ser Val Ser Cys  
235 1075 1080 1085  
237 Gly Asp Gly Ile Gln Arg Arg Asp Thr Cys Leu Gly Pro Gln Ala  
238 1090 1095 1100  
240 Gln Ala Pro Val Pro Ala Asp Phe Cys Gln His Leu Pro Lys Pro Val  
241 1105 1110 1115 1120  
243 Thr Val Arg Gly Cys Trp Ala Gly Pro Cys Val Gly Gln Gly Thr Pro  
244 1125 1130 1135  
246 Ser Leu Val Pro His Glu Glu Ala Ala Ala Pro Gly Arg Thr Thr Ala  
247 1140 1145 1150  
249 Thr Pro Ala Gly Ala Ser Leu Glu Trp Ser Gln Ala Arg Gly Leu Leu  
250 1155 1160 1165  
252 Phe Ser Pro Ala Pro Gln Pro Arg Arg Leu Leu Pro Gly Pro Gln Glu  
253 1170 1175 1180  
255 Asn Ser Val Gln Ser Ser Ala Cys Gly Arg Gln His Leu Glu Pro Thr  
256 1185 1190 1195 1200  
258 Gly Thr Ile Asp Met Arg Gly Pro Gln Ala Asp Cys Ala Val Ala  
259 1205 1210 1215  
261 Ile Gly Arg Pro Leu Gly Glu Val Val Thr Leu Arg Val Leu Glu Ser  
262 1220 1225 1230  
264 Ser Leu Asn Cys Ser Ala Gly Asp Met Leu Leu Leu Trp Gly Arg Leu  
265 1235 1240 1245  
267 Thr Trp Arg Lys Met Cys Arg Lys Leu Leu Asp Met Thr Phe Ser Ser  
268 1250 1255 1260  
270 Lys Thr Asn Thr Leu Val Val Arg Gln Arg Cys Gly Arg Pro Gly Gly  
271 1265 1270 1275 1280  
273 Gly Val Leu Leu Arg Tyr Gly Ser Gln Leu Ala Pro Glu Thr Phe Tyr  
274 1285 1290 1295  
276 Arg Glu Cys Asp Met Gln Leu Phe Gly Pro Trp Gly Glu Ile Val Ser  
277 1300 1305 1310  
279 Pro Ser Leu Ser Pro Ala Thr Ser Asn Ala Gly Gly Cys Arg Leu Phe  
280 1315 1320 1325  
282 Ile Asn Val Ala Pro His Ala Arg Ile Ala Ile His Ala Leu Ala Thr  
283 1330 1335 1340  
285 Asn Met Gly Ala Gly Thr Glu Gly Ala Asn Ala Ser Tyr Ile Leu Ile

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286	1345	1350	1355	1360
288	Arg Asp Thr His Ser Leu Arg Thr Thr Ala Phe His Gly Gln Gln Val			
289	1365	1370	1375	
291	Leu Tyr Trp Glu Ser Glu Ser Ser Gln Ala Glu Met Glu Phe Ser Glu			
292	1380	1385	1390	
294	Gly Phe Leu Lys Ala Gln Ala Ser Leu Arg Gly Gln Tyr Trp Thr Leu			
295	1395	1400	1405	
297	Gln Ser Trp Val Pro Glu Met Gln Asp Pro Gln Ser Trp Lys Gly Lys			
298	1410	1415	1420	
300	Glu Gly Thr			
301	1425			
304	<210> SEQ ID NO: 2			
305	<211> LENGTH: 30			
306	<212> TYPE: DNA			
307	<213> ORGANISM: Homo sapiens			
309	<400> SEQUENCE: 2			
310	ctggagcact acggcgcgcc cggcagcggc		30	
313	<210> SEQ ID NO: 3			
314	<211> LENGTH: 30			
315	<212> TYPE: DNA			
316	<213> ORGANISM: Homo sapiens			
318	<400> SEQUENCE: 3			
319	atgtgcaaca ctcaggcctg cgagaagacc		30	
322	<210> SEQ ID NO: 4			
323	<211> LENGTH: 30			
324	<212> TYPE: DNA			
325	<213> ORGANISM: Homo sapiens			
327	<400> SEQUENCE: 4			
328	ccaacctgac cagtgtctac attgccaacc		30	
331	<210> SEQ ID NO: 5			
332	<211> LENGTH: 21			
333	<212> TYPE: DNA			
334	<213> ORGANISM: Homo sapiens			
336	<400> SEQUENCE: 5			
337	ctggagccct gcccacctag g		21	
340	<210> SEQ ID NO: 6			
341	<211> LENGTH: 62			
342	<212> TYPE: DNA			
343	<213> ORGANISM: Homo sapiens			
345	<400> SEQUENCE: 6			
346	tccgtcgact cttatcactt atcgtcatcg tcctttagt cgtcccacac gcagcgcgcc	60		
347	cg		62	
350	<210> SEQ ID NO: 7			
351	<211> LENGTH: 62			
352	<212> TYPE: DNA			
353	<213> ORGANISM: Homo sapiens			
355	<400> SEQUENCE: 7			
356	tccgtcgact cttatcactt atcgtcatcg tcctttagt cgcgccatg cactgctgct	60		
357	at		62	

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:20; Xaa Pos. 3,4,6,7,9,10

**VERIFICATION SUMMARY**

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Input Set : A:\81356247.APP

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L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0